



1

SEQUENCE LISTING

<110> Kindsvogel, Wayne R.
Topouzis, Stavros

<120> SOLUBLE ZCYTOR11 CYTOKINE RECEPTORS

<130> 00-56

<150> US 60/223,827

<151> 2000-08-08

<150> US 60/250,876

<151> 2000-12-01

<160> 35

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2831

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (34)...(1755)

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Met Arg Thr Leu Leu Thr Ile
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ttg act gtg gga tcc ctg gct gct cac gcc cct gag gac ccc tcg gat
Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp
10 15 20

ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg
Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu
25 30 35

acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc
198

Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile				
40	45	50	55	
gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt				246
Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys				
60	65	70		
cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag acg ggc aac				294
Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn				
75	80	85		
ctc acg gag ctc tac tat gcc agg gtc acc gct gtc agt gcg gga ggc				342
Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly				
90	95	100		
cgg tca gcc acc aag atg act gac agg ttc agc tct ctg cag cac act				390
Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr				
105	110	115		
acc ctc aag cca cct gat gtg acc tgt atc tcc aaa gtg aga tcg att				438
Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile				
120	125	130	135	
cag atg att gtt cat cct acc ccc acg cca atc cgt gca ggc gat ggc				486
Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly				
140	145	150		
cac cgg cta acc ctg gaa gac atc ttc cat gac ctg ttc tac cac tta				534
His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu				
155	160	165		
gag ctc cag gtc aac cgc acc tac caa atg cac ctt gga ggg aag cag				582
Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln				
170	175	180		
aga gaa tat gag ttc ttc ggc ctg acc cct gac aca gag ttc ctt ggc				630
Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly				
185	190	195		
acc atc atg att tgc gtt ccc acc tgg gcc aag gag agt gcc ccc tac				678
Ihr Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr				
200	205	210	215	

atg tgc cga gtg aag aca ctg cca gac cgg aca tgg acc tac tcc ttc Met Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe	726
220 225 230	
tcc gga gcc ttc ctg ttc tcc atg ggc ttc ctc gtc gca gta ctc tgc Ser Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys	774
235 240 245	
tac ctg agc tac aga tat gtc acc aag ccc cct gca cct ccc aac tcc Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Pro Asn Ser	822
250 255 260	
ctg aac gtc cag cga gtc ctg act ttc cag ccg ctg ccc ilc atc cag Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln	870
265 270 275	
gag cac gtc ctg atc cct gtc ttt gac ctc agc ggc ccc agc agt ctg Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu	918
280 285 290 295	
gcc cag cct gtc cag tac tcc cag atc agg gtg tct gga ccc agg gag Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu	966
300 305 310	
ccc gca gga gct cca cag cgg cat agc ctg tcc gag atc acc tac tta Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu	1014
315 320 325	
ggg cag cca gac atc tcc atc ctc cag ccc tcc aac gtg cca cct ccc Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro	1062
330 335 340	
cag atc ctc tcc cca ctg tcc tat gcc cca aac gct gcc cct gag gtc Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val	1110
345 350 355	
ggg ccc cca tcc tat gca cct cag gtg acc ccc gaa gct caa ttc cca Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro	1158
360 365 370 375	
ttc tac gcc cca cag gcc atc tct aag gtc cag cct tcc tcc tat gcc Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala	1206
380 385 390	

cct caa gcc act ccg gac agc tgg cct ccc tcc tat ggg gta tgc atg Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met	395	400	405	1254	
gaa ggt tct ggc aaa gac tcc ccc act ggg aca ctt tct agt cct aaa Glu Gly Ser Gly Lys Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Lys	410	415	420	1302	
cac ctt agg cct aaa ggt cag ctt cag aaa gag cca cca gct gga agc His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser	425	430	435	1350	
tgc atg tta ggt ggc ctt tct ctg cag gag gtg acc tcc ttg gct atg Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met	440	445	450	455	1398
gag gaa tcc caa gaa gca aaa tca ttg cac cag ccc ctg ggg att tgc Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys	460	465	470	1446	
aca gac aga aca tct gac cca aat gtg cta cac agt ggg gag gaa ggg Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly	475	480	485	1494	
aca cca cag tac cta aag ggc cag ctc ccc ctc tcc tca gtc cag Thr Pro Gln Tyr Leu Lys Gly Gln Leu Pro Leu Leu Ser Ser Val Gln	490	495	500	1542	
atc gag ggc cac ccc atg tcc ctc cct ttg caa cct cct tcc ggt cca Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro	505	510	515	1590	
tgt tcc ccc tcc gac caa ggt cca agt ccc tgg ggc ctg ctg gag tcc Cys Ser Pro Ser Asp Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser	520	525	530	535	1638
ctt gtg tgt ccc aag gat gaa gcc aag agc cca gcc cct gag acc tca Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser	540	545	550	1686	
gac ctg gag cag ccc aca gaa ctg gat tct ctt ttc aga ggc ctg gcc				1734	

Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala
 555 560 565

ctg act gtg cag tgg gag tcc tgagggaat gggaaaggct tggtgcttcc 1785
 Leu Thr Val Gln Trp Glu Ser
 570

tccctgtccc taccaggatgt cacatcccttg gctgtcaatc ccatgcctgc ccatgccaca 1845
 cactctgcga tctggcctca gacgggtgcc ctggagagaa gcagagggag tggcatgcag 1905
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 gggagctctg gggagcagct tggtagaca agcgcgtgct cgctgagccc tgcaaggcag 2025
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<210> 2
 <211> 574
 <212> PRT
 <213> Homo sapien

<400> 2

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 Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
 20 25 30
 Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
 35 40 45
 Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
 50 55 60
 Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
 65 70 75 80
 Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val

85	90	95	
Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg			
100	105	110	
Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys			
115	120	125	
Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr			
130	135	140	
Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Gln Asp Ile Phe			
145	150	155	160
His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln			
165	170	175	
Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr			
180	185	190	
Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp			
195	200	205	
Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp			
210	215	220	
Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly			
225	230	235	240
Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys			
245	250	255	
Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe			
260	265	270	
Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp			
275	280	285	
Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro Val Gln Tyr Ser Gln Ile			
290	295	300	
Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Pro Gln Arg His Ser			
305	310	315	320
Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro Asp Ile Ser Ile Leu Gln			
325	330	335	
Pro Ser Asn Val Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala			
340	345	350	
Pro Asn Ala Ala Pro Glu Val Gln Pro Pro Ser Tyr Ala Pro Gln Val			
355	360	365	
Thr Pro Glu Ala Gln Phe Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys			
370	375	380	
Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro			
385	390	395	400
Pro Ser Tyr Gly Val Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr			
405	410	415	
Gly Thr Leu Ser Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln			
420	425	430	

Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln
 435 440 445
 Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu
 450 455 460
 His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val
 465 470 475 480
 Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu
 485 490 495
 Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro
 500 505 510
 Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser
 515 520 525
 Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys
 530 535 540
 Ser Pro Ala Pro Glu Thr Ser Asp Leu Glu Gln Pro Thr Glu Leu Asp
 545 550 555 560
 Ser Leu Phe Arg Gly Leu Ala Leu Thr Val Gln Trp Glu Ser
 565 570

<210> 3
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 <212> PRT
 <213> Homo sapiens

<400> 3

Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser Ser
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 Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro
 20 25 30
 Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp
 35 40 45
 Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu
 50 55 60
 Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr
 65 70 75 80
 Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg Phe
 85 90 95
 Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys Ile
 100 105 110
 Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr Pro
 115 120 125
 Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe His
 130 135 140

Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met
 145 150 155 160
 His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
 165 170 175
 Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp Ala
 180 185 190
 Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp Arg
 195 200 205
 Thr Trp Thr
 210

<?10> 4
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 <?12> PRT
 <?13> Artificial Sequence

<?20>
 <?23> Glu-Glu peptide tag

<400> 4
 Glu Tyr Met Pro Met Glu
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<?10> 5
 <?11> 8
 <?12> PRT
 <?13> Artificial Sequence

<?20>
 <?23> Flag-tag peptide

<400> 5
 Asp Tyr Lys Asp Asp Asp Lys
 1 5

<?10> 6
 <?11> 699
 <?12> DNA
 <?13> Homo sapiens

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 ggggcaccgt cagtcttcct cttccccca aaaccccaagg acaccctcat gatctcccg 120

| | |
|--|--|
| acccctgagg tcacatgcgt ggtggggac gtgagccacg aagaccctga ggtcaagtcc
aactggtacg tggacggcggt ggagggtgcgt aatgcctaaga caaagcccgcg ggaggaggcag
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
ggcaaggagt acaagtgcac ggtctccaac aaagccctcc catcctccat cgagaaaacc
atctccaaag ccaaaggcga gccccgagaa ccacagggtgt acaccctgcc cccatccccgg
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
cccgtgtgg actccgacgg ctccttcttc ctctacagca agctaccgt ggacaagagc
aggtggcagc agggaaacgt cttctcatgc tccgtatgc atgaggctct gcacaaccac
tacacgcaga agacccttc cctgtctccg gttaaataaa | 180
240
300
360
420
480
540
600
660
699 |
| <210> 7 | |
| <211> 1116 | |
| <212> DNA | |
| <213> homo sapiens | |
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| <222> (21)...(557) | |
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Met Ala Ala Leu Gln Ser Val Ser Ser Phe | 53 |
| 1 5 10 | |
| ctt atg ggg acc ctg gcc acc agc tgc ctc ctt ctc ttg gcc ctc ttg
Leu Met G`y Thr Leu Ala Thr Ser Cys Leu Leu Leu Ala Leu Leu | 101 |
| 15 20 25 | |
| gta cag gga gga gca gct gcg ccc atc agc tcc cac tgc agg ctt gac
Val Gln G`y Gly Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp | 149 |
| 30 35 40 | |
| aag tcc aac ttc cag cag ccc tat atc acc aac cgc acc ttc atg ctg
Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu | 197 |
| 45 50 55 | |
| gct aag gag gct agc ttg gct gat aac aac aca gac gtt cgt ctc att
Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile | 245 |
| 60 65 70 75 | |
| ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg | 293 |

| | | | |
|--|-----|-----|------|
| Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu | | | |
| 80 | 85 | 90 | |
| atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa | | | 341 |
| Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln | | | |
| 95 | 100 | 105 | |
| tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc | | | 389 |
| Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala | | | |
| 110 | 115 | 120 | |
| agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg | | | 437 |
| Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu | | | |
| 125 | 130 | 135 | |
| cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt | | | 485 |
| His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Leu | | | |
| 140 | 145 | 150 | 155 |
| gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt | | | 533 |
| Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe | | | |
| 160 | 165 | 170 | |
| atg tct ctg aga aat gcc tgc att tgaccagagc aaagctgaaa aatgaataac | | | 587 |
| Met Ser Leu Arg Asn Ala Cys Ile | | | |
| 175 | | | |
| taacccctt tccctgctag aaataacaat tagatgcccc aaagcgattt ttttaacca | | | 647 |
| aaaggaagat gggaaagccaa actccatcat gatgggtgga ttccaaatga acccctgcgt | | | 707 |
| tagttacaaa ggaaaccaat gccactttt gttataagac cagaaggtag actttctaa | | | 767 |
| catagatatt tattgataac atttcattgt aactgggttt ctatacacag aaaacaattt | | | 827 |
| attttttaaa taattgtctt ttccataaaa aaagattact ttccattcct ttagggaaa | | | 887 |
| aaacccctaa atagcttcat gttccataa tcagttactt atatttataa atgtattttat | | | 947 |
| tattattata agactgcatt ttatttataat cattttatta atatggattt atttatagaa | | | 1007 |
| acatcattcg atattgctac ttgagtgtaa ggctaataattt gatattttag acaataat | | | 1067 |
| tagagctata acatgtttat ttgacctcaa taaacacttg gatattccta | | | 1116 |

<210> 8
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 <212> PRT
 <213> homo sapiens

<400> 8

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 20 25 30
 Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln
 35 40 45
 Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
 50 55 60
 Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
 65 70 75 80
 His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
 85 90 95
 Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
 100 105 110
 Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
 115 120 125
 Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
 130 135 140
 Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
 145 150 155 160
 Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
 165 170 175
 Ala Cys Ile

<210> 9

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide prime ZC28590

<400> 9

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36

<210> 10

<211> 33

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide prime ZC28580

| | |
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| <210> 11 | |
| <211> 18 | |
| <212> DNA | |
| <213> Artificial Sequence | |
| <220> | |
| <223> Oligonucleotide prime ZC14666 | |
| <400> 11 | |
| agccaccaag atgactga | 18 |
| <210> 12 | |
| <211> 22 | |
| <212> DNA | |
| <213> Artificial Sequence | |
| <220> | |
| <223> Oligonucleotide prime ZC14742 | |
| <400> 12 | |
| tgcatttggc aggtgcgggt ga | 22 |
| <210> 13 | |
| <211> 6 | |
| <212> PRT | |
| <213> Artificial Sequence | |
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| <223> His tag | |
| <400> 13 | |
| His His His His His His | |
| 1 | 5 |
| <210> 14 | |
| <211> 63 | |
| <212> DNA | |
| <213> Artificial Sequence | |

<220>
 <223> Oligonucleotide primer ZC29239

<400> 14
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 tgc 63

<210> 15
 <211> 65
 <212> DNA
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<220>
 <223> Oligonucleotide primer ZC29232

<400> 15
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 gggag 65

<210> 16
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 <212> DNA
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<220>
 <223> Oligonucleotide primer ZC39319

<400> 16
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<210> 17
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 <212> DNA
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<220>
 <223> Oligonucleotide primer ZC39325

<400> 17
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<210> 18
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (660)

<400> 18

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Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser | 1 | 5 | 10 | 15 | 48 |
| gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt
Ala Leu Gly Met Val Pro Pro Glu Asn Val Arg Met Asn Ser Val | 20 | 25 | | 30 | 96 |
| aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly | 35 | 40 | | 45 | 144 |
| aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp | 50 | 55 | | 60 | 192 |
| aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca agt ctt tcc
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser | 65 | 70 | | 75 | 240 |
| aag tat ggt gac cac acc ttg aga gtc agg gct gaa ttt gca gat gag
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu | 85 | 90 | | 95 | 288 |
| cat tca gac tgg gta aac atc acc ttc tgt cct gtg gat gac acc att
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile | 100 | 105 | | 110 | 336 |
| att gga ccc cct gga atg caa gta gaa gta ctt gat gat tct tta cat
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His | 115 | 120 | | 125 | 384 |
| atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr | 130 | 135 | | 140 | 432 |

| | |
|---|-----|
| atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa | 480 |
| Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys | |
| 145 150 155 160 | |
| aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag | 528 |
| Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu | |
| 165 170 175 | |
| gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga | 576 |
| Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg | |
| 180 185 190 | |
| ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc | 624 |
| Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val | |
| 195 200 205 | |
| tgt gag caa aca acc cat gac gaa acg gtc ccc tcc | 660 |
| Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser | |
| 210 215 220 | |

<210> 19
 <211> 220
 <212> PRT
 <213> Homo sapiens

<400> 19
 Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1 5 10 15
 Ala Leu G^y Met Val Pro Pro Glu Asn Val Arg Met Asn Ser Val
 20 25 30
 Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
 35 40 45
 Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
 50 55 60
 Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
 65 70 75 80
 Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
 85 90 95
 His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
 100 105 110

Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
 115 120 125
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
 130 135 140
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
 145 150 155 160
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
 165 170 175
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
 180 185 190
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
 195 200 205
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
 210 215 220

<210> 20

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC38931

<400> 20

acaaagccgc gggaggag 18

<210> 21

<211> 82

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39042

<400> 21

ctgactcgag tcagtatgg tcatggatgg ggcacactga tccggaaacca cgccggaaacca 60
 gtttacccgg aqacaggag ag 82

<210> 22

<211> 1428

<212> DNA

<213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(1428)

<223> CRF2-4 extracellular cytokine binding domain fused
 to IgG1 with a 6-HIS tag

| | | | | | | | | | | | | | | | | | |
|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| <400> 22 | | | | | | | | | | | | | | | | | |
| atg | gcg | tgg | agt | ctt | ggg | agc | tgg | ctg | ggt | ggc | tgc | ctg | ctg | gtg | tca | | 48 |
| Met | Ala | Trp | Ser | Leu | Gly | Ser | Trp | Leu | Gly | Gly | Cys | Leu | Leu | Val | Ser | | |
| 1 | | | 5 | | | | | 10 | | | | | | 15 | | | |
| gca | ttg | gga | atg | gta | cca | cct | ccc | gaa | aat | gtc | aga | atg | aat | tct | gtt | | 96 |
| Ala | Leu | Gly | Met | Val | Pro | Pro | Pro | Glu | Asn | Val | Arg | Met | Asn | Ser | Val | | |
| | | | 20 | | | | | 25 | | | 30 | | | | | | |
| aat | ttc | aag | aac | att | cta | cag | tgg | gag | tca | cct | gct | ttt | gcc | aaa | ggg | | 144 |
| Asn | Phe | Lys | Asn | Ile | Leu | Gln | Trp | Glu | Ser | Pro | Ala | Phe | Ala | Lys | Gly | | |
| | | | 35 | | | | | 40 | | | 45 | | | | | | |
| aac | ctg | act | ttc | aca | gct | cag | tac | cta | agt | tat | agg | ata | ttc | caa | gat | | 192 |
| Asn | Leu | Thr | Phe | Thr | Ala | Gln | Tyr | Leu | Ser | Tyr | Arg | Ile | Phe | Gln | Asp | | |
| | | | 50 | | | | | 55 | | | 60 | | | | | | |
| aaa | tgc | atg | aat | act | acc | ttg | acg | gaa | tgt | gat | ttc | tca | agt | ctt | tcc | | 240 |
| Lys | Cys | Met | Asn | Thr | Thr | Leu | Thr | Glu | Cys | Asp | Phe | Ser | Ser | Leu | Ser | | |
| | | | 65 | | | 70 | | | 75 | | | 80 | | | | | |
| aag | tat | ggt | gac | cac | acc | ttg | aga | gtc | agg | gct | gaa | ttt | gca | gat | gag | | 288 |
| Lys | Tyr | Gly | Asp | His | Thr | Leu | Arg | Val | Arg | Ala | Glu | Phe | Ala | Asp | Glu | | |
| | | | | | 85 | | | | 90 | | | 95 | | | | | |
| cat | tca | gac | tgg | gta | aac | atc | acc | ttc | tgt | cct | gtg | gat | gac | acc | att | | 336 |
| His | Ser | Asp | Trp | Val | Asn | Ile | Thr | Phe | Cys | Pro | Val | Asp | Asp | Thr | Ile | | |
| | | | | | 100 | | | 105 | | | 110 | | | | | | |
| att | gga | ccc | cct | gga | atg | caa | gta | gaa | gta | ctt | gat | gat | tct | tta | cat | | 384 |
| Ile | Gly | Pro | Pro | Gly | Met | Gln | Val | Glu | Val | Leu | Asp | Asp | Ser | Leu | His | | |
| | | | | | 115 | | | 120 | | | 125 | | | | | | |
| atg | cgt | ttc | tta | gcc | cct | aaa | att | gag | aat | gaa | tac | gaa | act | tgg | act | | 432 |
| Met | Arg | Phe | Leu | Ala | Pro | Lys | Ile | Glu | Asn | Glu | Tyr | Glu | Thr | Trp | Thr | | |
| | | | | | 130 | | | 135 | | | 140 | | | | | | |

| | |
|---|-----|
| atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa | 480 |
| Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys | |
| 145 150 155 160 | |
| aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag | 528 |
| Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu | |
| 165 170 175 | |
| gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga | 576 |
| Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg | |
| 180 185 190 | |
| ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc | 624 |
| Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val | |
| 195 200 205 | |
| tgt gag caa aca acc cat gac gaa acg gtc ccc tcc gga tcc ggt tcg | 672 |
| Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser | |
| 210 215 220 | |
| ggt tcg ggt tcg gag ccc aga tca tca gac aaa act cac aca tgc cca | 720 |
| Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro | |
| 225 230 235 240 | |
| ccg tgc cca gca cct gaa gcc gag ggg gca ccg tca gtc ttc ctc ttc | 768 |
| Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe | |
| 245 250 255 | |
| ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc | 816 |
| Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val | |
| 260 265 270 | |
| aca tgc gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc | 864 |
| Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe | |
| 275 280 285 | |
| aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg | 912 |
| Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro | |
| 290 295 300 | |
| cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc | 960 |

| | | | | |
|---|-----|-----|-----|------|
| Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr | | | | |
| 305 | 310 | 315 | 320 | |
| gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc | | | | 1008 |
| Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val | | | | |
| 325 | 330 | 335 | | |
| tcc aac aaa gcc ctc cca tcc atc gag aaa acc atc tcc aaa gcc | | | | 1056 |
| Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala | | | | |
| 340 | 345 | 350 | | |
| aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg | | | | 1104 |
| Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg | | | | |
| 355 | 360 | 365 | | |
| gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc | | | | 1152 |
| Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly | | | | |
| 370 | 375 | 380 | | |
| ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg | | | | 1200 |
| Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro | | | | |
| 385 | 390 | 395 | 400 | |
| gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc | | | | 1248 |
| Glu Asn Asn Tyr Lys Thr Pro Pro Val Leu Asp Ser Asp Gly Ser | | | | |
| 405 | 410 | 415 | | |
| ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag | | | | 1296 |
| Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln | | | | |
| 420 | 425 | 430 | | |
| ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac | | | | 1344 |
| Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His | | | | |
| 435 | 440 | 445 | | |
| tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa ctg gtt ccg cgt | | | | 1392 |
| Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg | | | | |
| 450 | 455 | 460 | | |
| ggt tcc gga tca ggt ggc cat cac cat cac cat cac | | | | 1428 |
| Gly Ser Gly Ser Gly Gly His His His His His His | | | | |
| 465 | 470 | 475 | | |

<210> 23
 <211> 476
 <212> PRT
 <213> Homo sapiens

<400> 23
 Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1 5 10 15
 Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
 20 25 30
 Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
 35 40 45
 Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
 50 55 60
 Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
 65 70 75 80
 Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
 85 90 95
 His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
 100 105 110
 Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
 115 120 125
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
 130 135 140
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
 145 150 155 160
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
 165 170 175
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
 180 185 190
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
 195 200 205
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser
 210 215 220
 Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro
 225 230 235 240
 Pro Cys Pro Ala Pro Gln Ala Glu Gly Ala Pro Ser Val Phe Leu Phe
 245 250 255
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 260 265 270
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 275 280 285

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 290 295 300
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 305 310 315 320
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 325 330 335
 Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
 340 345 350
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 355 360 365
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 370 375 380
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 385 390 395 400
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 405 410 415
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 420 425 430
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 435 440 445
 Tyr Thr Gln Lys Ser Leu Ser Pro Gly Lys Leu Val Pro Arg
 450 455 460
 Gly Ser Gly Ser Gly His His His His His His
 465 470 475

<210> 24

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC29328

<400> 24

| | |
|---|----|
| tcagaggat cccgttcggg ttccgggttcg gagcccatat | 60 |
| tgc | 63 |

<210> 25

<211> 65

<212> DNA

<213> Artificial Sequence

<220>

<?> Oligonucleotide primer ZC29231

<400> 25

cgactgactc gagctactcc ataggcatat actcgccacc tgcaccccttta cccggagaca 60
gggag 65

<210> 26

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39335

<400> 26

atcggaaatc gcagaagcca tgaggacgct gctgaccatc ttgactgtgg ggtccctggc 60
tgctcacgcc 70

<210> 27

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC28981

<400> 27

tttgggcctcc ctgagctctg gtggaa 26

<210> 28

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39043

<400> 28

ctgactcgag ctactccata ggcataatact cgccacactga tccggaaacca cgcgaaacca 60
gtttaccggg aqacaggag 80

<210> 29

<211> 1452

<212> DNA

<213> Artificial Sequence

<220>

<223> hzcytor11 extracellular cytokine binding domain
fused to IgG1 with a Glu-Glu tag

<221> CDS

<222> (1)...(1452)

<400> 29

atg	agg	acg	ctg	ctg	acc	atc	ttg	act	gtg	gga	tcc	ctg	gct	gct	cac	48
Met	Arg	Thr	Leu	Leu	Thr	Ile	Leu	Thr	Val	Gly	Ser	Leu	Ala	Ala	His	
1						5						10			15	
gcc	cct	gag	gac	ccc	tcg	gat	ctg	ctc	cag	cac	gtg	aaa	ttc	cag	tcc	96
Ala	Pro	Glu	Asp	Pro	Ser	Asp	Leu	Leu	Gln	His	Val	Lys	Phe	Gln	Ser	
						20						25			30	
agc	aac	ttt	gaa	aac	atc	ctg	acg	tgg	gac	agc	ggg	cca	gag	ggc	acc	144
Ser	Asn	Phe	Glu	Asn	Ile	Leu	Thr	Trp	Asp	Ser	Gly	Pro	Glu	Gly	Thr	
						35			40			45				
cca	gac	acg	gtc	tac	agc	atc	gag	tat	aag	acg	tac	gga	gag	agg	gac	192
Pro	Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp	
						50			55			60				
tgg	gtg	gca	aag	aag	ggc	tgt	cag	cgg	atc	acc	cgg	aag	tcc	tgc	aac	240
Trp	Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn	
						65			70			75			80	
ctg	acg	gtg	gag	acg	ggc	aac	ctc	acg	gag	ctc	tac	tat	gcc	agg	gtc	288
Leu	Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val	
						85			90			95				
acc	gct	gtc	agt	gct	gga	ggc	cg	tca	gcc	acc	aag	atg	act	gac	agg	336
Thr	Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg	
						100			105			110				
ttc	agc	tct	ctg	cag	cac	act	acc	ctc	aag	cca	cct	gat	gtg	acc	tgt	384
Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys	
						115			120			125				

atc tcc aaa gtg aga tgc att cag atg att gtt cat cct acc ccc acg Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr 130 135 140	432
cca atc cgt gca ggc gat ggc cac cgg cta acc ctg gaa gac atc ttc Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe 145 150 155 160	480
cat gac ctg ttc tac cac tta gag ctc cag gtc aac cgc acc tac caa His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln 165 170 175	528
atg cac ctt gga ggg aag cag aga gaa tat gag ttc ttc ggc ctg acc Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr 180 185 190	576
cct gac aca gag ttc ctt ggc acc atc atg att tgc gtt ccc acc tgg Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp 195 200 205	624
gcc aag gag agt gcc ccc tac atg tgc cga gtg aag aca ctg cca gac Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp 210 215 220	672
cgg aca tgg acc gga tcc ggt tcg ggt tcg gag ccc aga tca Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser 225 230 235 240	720
tca gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa gcc gag Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu 245 250 255	768
ggg gca ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu 260 265 270	816
atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser 275 280 285	864
cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu 290 295 300	912

gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac aac agc acg			960
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr			
305	310	315	320
tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat			1008
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn			
325	330	335	
ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca tcc tcc			1056
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser			
340	345	350	
atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag			1104
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln			
355	360	365	
gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc			1152
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val			
370	375	380	
agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtc			1200
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val			
385	390	395	400
gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct			1248
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro			
405	410	415	
ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc			1296
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr			
420	425	430	
gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtc			1344
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val			
435	440	445	
atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg			1392
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu			
450	455	460	
tct ccg ggt aaa ctg gtt ccg cgt ggt tcc gga tca ggt ggc gag tat			1440

Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Glu Tyr
 465 470 475 480

atg cct atg gag 1452
 Met Pro Met Glu

<210> 30
 <211> 484
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hzcytor11 extracellular cytokine binding domain
 fused to IgGg1 with a Glu-Glu tag

<400> 30
 Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
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 Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
 20 25 30
 Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
 35 40 45
 Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
 50 55 60
 Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
 65 70 75 80
 Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
 85 90 95
 Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
 100 105 110
 Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
 115 120 125
 Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
 130 135 140
 Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
 145 150 155 160
 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
 165 170 175
 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
 180 185 190

Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
 195 200 205
 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
 210 215 220
 Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser
 225 230 235 240
 Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
 245 250 255
 Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 260 265 270
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 275 280 285
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 290 295 300
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Gln Tyr Asn Ser Thr
 305 310 315 320
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 325 330 335
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser
 340 345 350
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 355 360 365
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 370 375 380
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 385 390 395 400
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 405 410 415
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 420 425 430
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 435 440 445
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 450 455 460
 Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Glu Tyr
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 Met Pro Met Glu

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Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly	Asn	Leu	Thr
					20			25			30				
Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp	Lys	Cys	Met
					35			40			45				
Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser	Lys	Tyr	Gly
					50			55			60				
Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu	His	Ser	Asp
65					70			75			80				
Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile	Ile	Gly	Pro
					85			90			95				
Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Ala	Asp	Ser	Leu	His	Met	Arg	Phe
					100			105			110				
Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr	Met	Lys	Asn
					115			120			125				
Val	Tyr	Asn	Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys	Asn	Gly	Thr
					130			135			140				

Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg
 145 150 155 160
 Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu
 165 170 175
 Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln
 180 185 190
 Thr Thr His Asp Glu Thr Val
 195

<210> 34
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 <213> Homo sapiens

<400> 34

Ser Asp Ala His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe
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 Glu Ala Glu Phe Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn
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 Gln Ser Glu Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile
 35 40 45
 Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp
 50 55 60
 Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala
 65 70 75 80
 Arg Val Arg Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr
 85 90 95
 Asn Thr Arg Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val
 100 105 110
 Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro
 115 120 125
 Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser
 130 135 140
 His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe
 145 150 155 160
 Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr
 165 170 175
 Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala
 180 185 190
 Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu
 195 200 205
 Thr Arg Gln
 210

<210> 35
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<400> 35
 Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
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 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly
 20 25 30
 Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
 35 40 45
 Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
 50 55 60
 Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr
 65 70 75 80
 Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser
 85 90 95
 Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
 100 105 110
 Gly Met Glu Ile Thr Lys Asp Gly Phe His Leu Val Ile Glu Leu Glu
 115 120 125
 Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Arg Arg Glu
 130 135 140
 Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
 145 150 155 160
 Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
 165 170 175
 Gln Thr Phe Val Lys Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr
 180 185 190
 Glu Cys Val Glu Val Gln Gly Glu Ala
 195 200